



## SEQUENCE LISTING

10/503257

10 Nov 2004

15 NOV 2004

The Government of the United States of America, as represented by the Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention Chang, Gwong-Jen J.

<120> NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION

<130> 6395-64909-02

<140> 10/500,796

<141> 2004-07-06

<150> PCT/US02/10764

<151> 2002-04-04

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

<160> 61

<170> PatentIn version 3.3

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<223> Description of artificial sequence; note = synthetic construct

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<221> misc\_feature

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10/500796 #73

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Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala	
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Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	
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aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga	1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	
45 50 55 60	
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Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
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Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
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Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
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Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val	
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tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct	1335
Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
125 130 135 140	
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Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
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Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
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agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300			1815
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aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn 335 340 345			1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360			2007
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr 365 370 375 380			2055
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Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys			
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tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct			2391
Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala			
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ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg			2439
Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala			
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aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc			2487
Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser			
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Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala			
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Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro			
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Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu			
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ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag			2679
Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln			
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Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe			
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Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr			
	605	610	615
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Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys			
	625	630	635
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Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly			
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Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met			
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Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr			

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20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys

50

55

60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val  
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
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Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
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Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu

290

295

300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
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Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
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Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr  
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Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
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Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
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Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
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Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn  
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Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser  
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Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala  
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Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly  
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His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr  
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530

535

540

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Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His  
 580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu  
 595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe  
 610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln  
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Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile  
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Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala  
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Val Phe Leu Ala Thr Asn Val His Ala  
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&lt;210&gt; 12

&lt;211&gt; 46

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of artificial sequence; note = synthetic construct

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(46)

&lt;223&gt; WN 466

&lt;400&gt; 12

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46

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<223> CWN2444

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<220>  
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

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tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360

cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggag tatttacggg aaactgcccc cttggcagta catcaagtgt 480

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atgcccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca 600

tcgctattac catggtgatg cggtttttgg cagtacatca atgggcgtgg atagcggttt 660

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caaaatcaac gggactttcc aaaatgtcgt aacaactccg cccattgac gcaaattggc 780

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Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn  
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Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp  
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gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga 1093  
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg  
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cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc 1189  
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys  
80 85 90

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His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
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Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
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Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
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Met Gln Arg Val Val Phe Val Val Leu Leu Leu Val Ala Pro Ala	
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Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
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Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
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Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
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Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
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Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
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Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
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Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln	
335 340 345	



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Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly	
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Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His	
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<220>  
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Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr  
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Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp  
 50 55 60

Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu  
 65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser  
 85 90 95

Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg  
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Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu  
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Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr  
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Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu  
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Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg  
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Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe  
 180 185 190

Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly  
 195 200 205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile  
 210 215 220

Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu  
 225 230 235 240

Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val  
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Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His  
 260 265 270

Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val  
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Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
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Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr  
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Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
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Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala  
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Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg  
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Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys  
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Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp  
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Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu  
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Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser  
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Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu  
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Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
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Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala  
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Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
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Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly  
580 585 590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg  
595 600 605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly  
610 615 620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
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Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val  
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<210> 17

<211> 5334

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          Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
          1             5             10

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Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
          15             20             25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
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aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
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Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu

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tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605 610 615 620			2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635			2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650			2871
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Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
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Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
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Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
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Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
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Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
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His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
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Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
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Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
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Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val  
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Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
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Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
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Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
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Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
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Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
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Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
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Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
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Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
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Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
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Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr  
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Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
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Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
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Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
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Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His  
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Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn  
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Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala  
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His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr  
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Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala  
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Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser  
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Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp  
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Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr  
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Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly  
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Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu  
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Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe  
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Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln  
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Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile  
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Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala  
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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
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Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp  
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Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser  
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Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
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Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
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Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
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Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
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Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His	
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Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
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Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
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Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro	
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Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro	
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Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val	
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Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu  
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Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu  
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Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys  
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Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg  
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Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg  
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Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val  
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Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val  
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Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr  
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His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg

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Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser				
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Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr				
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Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu				
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Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly				
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Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys				
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Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr				
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Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly				
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Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln				
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Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly				
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Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln				
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Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala				
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Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys				
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His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe				
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Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln				

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440

445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val  
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Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val  
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Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp  
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Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg  
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Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala  
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Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Gly Phe  
 545 550 555 560

Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp  
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Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe  
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Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His  
 595 600 605

Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val Gly Lys  
 610 615 620

Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly  
 625 630 635 640

Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu  
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<223> Description of artificial sequence; note = synthetic construct

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Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
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Asn	Asn	Lys	Val	Met	Ile	Glu	Val	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr		
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Ile	Val	Val	Gly	Arg	Gly	Thr	Thr	Gln	Ile	Asn	Tyr	His	Trp	His	Lys		
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gag	gga	agc	agc	att	ggg	aag	gct	ttg	gcg	acc	aca	tgg	aaa	gga	gcc	2727	
Glu	Gly	Ser	Ser	Ile	Gly	Lys	Ala	Leu	Ala	Thr	Thr	Trp	Lys	Gly	Ala		
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Gln	Arg	Leu	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile		
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gga	gga	gtt	ttc	aat	tca	att	ggc	aaa	gct	gtc	cac	caa	gtt	ttc	gga	2823	
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cta	ctt	gga	gct	ctt	ctc	ctg	tgg	atg	ggg	ttg	cag	gcc	cgc	gac	agg	2919	
Leu	Leu	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Leu	Gln	Ala	Arg	Asp	Arg		
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agc	atc	tcg	ctg	act	cta	ctg	gct	gtc	gga	ggg	att	ctc	atc	ttt	ctg	2967	
Ser	Ile	Ser	Leu	Thr	Leu	Leu	Ala	Val	Gly	Gly	Ile	Leu	Ile	Phe	Leu		
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Ala	Thr	Ser	Val	Gln	Ala												
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Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn  
 35 40 45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp  
 50 55 60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu  
 65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu  
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Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg  
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Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu  
 115 120 125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr  
 130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu  
 145 150 155 160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg  
 165 170 175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe  
 180 185 190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly  
 195 200 205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val  
 210 215 220

Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu  
 225 230 235 240

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu  
 245 250 255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His  
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Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val  
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Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
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Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr  
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Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys  
 340 345 350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr  
 355 360 365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg  
 370 375 380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys  
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Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp  
 405 410 415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu  
 420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser  
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Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr  
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Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg  
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Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys  
 485 490 495

Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly  
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Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly  
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Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn  
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Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly  
 580 585 590

Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg  
 595 600 605

Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 610 615 620

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile  
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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
1 5 10  
ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999  
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys  
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Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr	
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ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag	1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys	
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Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro	
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aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac	1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn	
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Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg	
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tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag	1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys	
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Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu	
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caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg	1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr	
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Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val	
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gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac	1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His	
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tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga	1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly	
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act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg	1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met	
210 215 220	
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att	1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile	
225 230 235	
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Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr	
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His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
255 260 265 270	



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Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
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Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val	
305 310 315	
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Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly	
320 325 330	
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Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp	
335 340 345 350	
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct	2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala	
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Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr	
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Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala	
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Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile	
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Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu	
465 470 475	
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Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe	
480 485 490	
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Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val	
495 500 505 510	

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Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp	
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Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro	
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Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro	
545 550 555	
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Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr	
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Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln	
575 580 585 590	
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg	2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp	
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His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn	
625 630 635	
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Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile	
640 645 650	
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655 660 665 670	
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gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc	4832
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aacaggaagg caaaatgccg caaaaaaggg aataaggcg acacggaaat gttgaatact	5132
catactcttc ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg	5192
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 <212> PRT  
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<220>  
 <223> Synthetic Construct

<400> 24

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 1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg  
 20 25 30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser  
 35 40 45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp  
 50 55 60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu  
 65 70 75 80

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg  
 85 90 95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg  
 100 105 110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg  
 115 120 125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys  
 130 135 140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu  
 145 150 155 160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile  
 165 170 175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile  
 180 185 190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp  
 195 200 205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro  
 210 215 220

Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg  
 225 230 235 240

Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val  
 245 250 255

Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu  
 260 265 270

Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly  
 275 280 285

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
 290 295 300

Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
 305 310 315 320

Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
 325 330 335

Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
 340 345 350

Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
 355 360 365

Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
 370 375 380

Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
 385 390 395 400

Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met  
 405 410 415

His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val  
 420 425 430

Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
 435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu  
 450 455 460

His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu  
 465 470 475 480

Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys  
 485 490 495

Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val  
 500 505 510

Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu  
 515 520 525

Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala  
 530 535 540

Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly  
 545 550 555 560

Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln  
 565 570 575

Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met  
 580 585 590

Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe  
 595 600 605

Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr  
 610 615 620

Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile  
 625 630 635 640

Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr  
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Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met  
 660 665 670

Met Phe Leu Ser Leu Gly Val Gly Ala  
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<223> POW 454

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<223> CPOW 2417

<400> 26  
actggtaccc tcaaccccggt actcgccggc gaaaaagaaa a 41

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<220>  
<221> misc\_feature  
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<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
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Val Val Ile Ala Gly Thr Ser Ala  
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<210> 28  
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<223> YF 482

<400> 28  
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<223> CYF 2433

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<223> SLE 463

<400> 30  
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<210> 31  
<211> 40



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 <220>  
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 <223> CSLE 2477  
  
 <400> 31  
 accggttggtc gcacgttcgg actcgccggc gaaaaagaaa 40  
  
 <210> 32  
 <211> 39  
 <212> PRT  
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 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
 <400> 32  
  
 Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg  
 1 5 10 15  
  
 Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln  
 20 25 30  
  
 Leu Leu Ser Thr Tyr Gln Gly  
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 <210> 33  
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 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
 <400> 33  
  
 Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met  
 1 5 10 15  
  
 Lys Leu Ser Asn Phe Gln Gly Lys  
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 <210> 34  
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<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 34

Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile  
1 5 10 15

Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys  
20 25 30

<210> 35

<211> 39

<212> PRT

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<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 35

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met  
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys  
20 25 30

Leu Ser Asn Phe Gln Gly Lys  
35

<210> 36

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 36

Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile  
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Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln  
20 25 30

Gly Lys

<210> 37

<211> 33

<212> PRT  
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<220>  
<223> Description of artificial sequence; note = synthetic construct

<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly  
20 25 30

Lys

<210> 38  
<211> 46  
<212> PRT  
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<220>  
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<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn  
1 5 10 15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile  
20 25 30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu  
35 40 45

<210> 39  
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<212> PRT  
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<400> 39

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp  
1 5 10 15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala  
20 25 30

Thr Val Arg Lys Glu Arg Gly Asp  
 35 40

<210> 40  
 <211> 24  
 <212> PRT  
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Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala  
 1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp  
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<210> 41  
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 <212> PRT  
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 1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp  
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<210> 42  
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<220>  
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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

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cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
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Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
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Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	

cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
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Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	
195 200 205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg	1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	
210 215 220	
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Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
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Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
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Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggg tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	

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Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
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Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	
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Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	
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Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg	
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Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile	
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 gtgttatcac tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta 4824  
 agatgctttt ctgtgactgg tgagtactca accaagtcac tctgagaata gtgtatgcgg 4884  
 cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact 4944  
 ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg 5004  
 ctgttgagat ccagttcgat gtaaccact cgtgcaccca actgatcttc agcatctttt 5064  
 actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaagga 5124  
 ataagggcga cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc 5184  
 atttatcagg gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa 5244  
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<210> 43  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 43

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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly  
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu  
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp  
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu  
65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser  
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg  
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu  
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val  
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met  
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala  
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg  
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly  
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met  
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala  
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr  
245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu  
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp  
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val  
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val  
 305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly  
 325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile  
 340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr  
 355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn  
 370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg  
 385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr  
 405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn  
 420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly  
 435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser  
 450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp  
 465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe  
 485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile  
 500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu  
 515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val  
 530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu  
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln  
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe  
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr  
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys  
610 615 620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly  
625 630 635 640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile  
645 650 655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val  
660 665 670

Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala  
675 680 685

<210> 44  
<211> 5293  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note = synthetic construct

<220>  
<221> CDS  
<222> (910)..(2964)

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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120  
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180  
ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240  
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300

tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc	360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggag tattttacggt aaactgccc cttggcagta catcaagtgt	480
atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcttggcatt	540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgt acaactccgc cccattgacg caaatgggcg	780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc	900
gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	

atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	
195 200 205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg	1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	
210 215 220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca	1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa	2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	
435 440 445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg	2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	
450 455 460	
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga	2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg	
465 470 475	
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga	2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly	
480 485 490	
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata	2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile	
495 500 505 510	
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct	2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro	
515 520 525	
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att	2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile	
530 535 540	
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa	2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu	
545 550 555	
gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg	2631
Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro	
560 565 570	
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa	2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln	
575 580 585 590	
atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt	2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly	
595 600 605	
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata	2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile	
610 615 620	
gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt	2823
Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe	
625 630 635	

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc	2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu	
640 645 650	
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta	2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu	
655 660 665 670	
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct	2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala	
675 680 685	
taattagttt gggcgggcgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc	3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg	3084
tttgccctc ccccgctgct tccttgacct tggaagggtgc cactccact gtcctttcct	3144
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cgggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg	3324
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caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga	3564
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cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggttaag	3864
acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggatatgt	3924
aggcgggtgct acagagttct tgaagtgggt gcctaactac ggctacacta gaagaacagt	3984
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atccggcaaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc agcagattac	4104
gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacgggggt ctgacgctca	4164
gtggaacgaa aactcacgtt aagggtttt ggtcatgaga ttatcaaaaa ggatcttcac	4224
ctagatcctt ttaaattaaa aatgaagttt taaatcaatc taaagtatat atgagtaaac	4284
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tcgttcaccc atagttgctt gactccccgt cgtgtagata actacgatac gggagggtt	4404



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accatctggc cccagtgtg caatgatacc gcgagaccca cgctcaccgg ctccagattt 4464
atcagcaata aaccagccag ccggaagggc cgagcgcaga agtgggtcctg caactttatc 4524
cgccctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa 4584
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catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244
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<210> 45
<211> 685
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 45

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
          20           25           30

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
          35           40           45

```

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Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
          50           55           60

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Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65           70           75           80

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Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser  
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg  
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu  
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val  
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met  
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala  
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg  
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly  
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met  
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala  
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr  
245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu  
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp  
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val  
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val  
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly  
325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile  
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr  
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn  
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg  
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr  
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn  
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly  
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser  
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp  
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe  
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile  
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu  
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val  
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu  
545 550 555 560

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln  
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe  
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr  
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys  
610 615 620

Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly  
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met  
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr  
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala  
675 680 685

<210> 46  
<211> 5293  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note = synthetic construct

<220>  
<221> CDS  
<222> (910) .. (2964)

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180  
ttagggtag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240  
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300  
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360

cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccataa gggactttcc 420  
 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt 480  
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540  
 atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600  
 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660  
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720  
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggag 780  
 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840  
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc 900  
 gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951  
           Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
           1                  5                          10  
 ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999  
 Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg  
 15                  20                  25                  30  
 aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047  
 Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser  
                   35                  40                  45  
 ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc 1095  
 Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala  
                   50                  55                  60  
 atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc 1143  
 Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro  
           65                  70                  75  
 ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct 1191  
 Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser  
           80                  85                  90  
 acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat 1239  
 Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His  
 95                  100                  105                  110  
 aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga 1287  
 Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly  
           115                  120                  125  
 ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa 1335  
 Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys  
           130                  135                  140  
 cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc 1383  
 His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr  
           145                  150                  155  
 atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa 1431  
 Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln

160	165	170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca			1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr			
175	180	185	190
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca			1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser			
	195	200	205
gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg			1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr			
	210	215	220
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca			1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr			
	225	230	235
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag			1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys			
	240	245	250
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc			1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro			
	255	260	265
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg			1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met			
	275	280	285
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc			1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly			
	290	295	300
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa			1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys			
	305	310	315
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac			1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His			
	320	325	330
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag			1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys			
	335	340	345
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca			2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr			
	355	360	365
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac			2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp			
	370	375	380
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg			2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val			
	385	390	395
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg			2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala			

400	405	410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430			2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln 435 440 445			2247
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met 450 455 460			2295
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg 465 470 475			2343
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490			2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510			2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525			2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540			2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555			2583
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro 560 565 570			2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys 575 580 585 590			2679
gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly 595 600 605			2727
gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile 610 615 620			2775
gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe 625 630 635			2823
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu 640 645 650			2871

640	645	650	
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta			2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu			
655	660	665	670
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct			2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala			
	675	680	685
taattagttt gagcgggcgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc			3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg			3084
tttgcccctc ccccgtagct tccttgaccc tggaaggtgc cactcccact gtcctttcct			3144
aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg			3204
gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg			3264
cgggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg			3324
cgcggggaga ggcggtttgc gtattgggcg ctcttcgctt tcctcgctca ctgactcgct			3384
gcgctcggtc gttcggtgc ggcgagcgg atcagctcac tcaaaggcgg taatacggtt			3444
atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc			3504
caggaaccgt aaaaaggccg cggtgctggc gtttttccat aggctccgcc cccctgacga			3564
gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata			3624
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gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacgggggt ctgacgctca			4164
gtggaacgaa aactcacggt aagggtttt ggtcatgaga ttatcaaaaa ggatcttcac			4224
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accatctggc cccagtgtg caatgatacc gcgagaccca cgctcaccgg ctccagattt			4464



atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggctctg caactttatc 4524  
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 tagtttgccc aacgttggtg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg 4644  
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 aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5184  
 ctttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244  
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 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

<400> 47

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
 1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly  
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu  
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp  
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu  
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg  
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu  
115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val  
130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met  
145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala  
165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg  
180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly  
195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met  
210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala  
225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr  
245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu  
260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp  
275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val  
290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val  
305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly

325

330

335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile  
 340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr  
 355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn  
 370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg  
 385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr  
 405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn  
 420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly  
 435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser  
 450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp  
 465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe  
 485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile  
 500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu  
 515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val  
 530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu  
 545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln

565

570

575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe  
 580 585 590

Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr  
 595 600 605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys  
 610 615 620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly  
 625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met  
 645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr  
 660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala  
 675 680 685

&lt;210&gt; 48

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of artificial sequence; note = synthetic construct

&lt;400&gt; 48

tgtgcaggcg ccttcattt aaccacacgt aacg

34

&lt;210&gt; 49

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of artificial sequence; note = synthetic construct

&lt;400&gt; 49

tcgagcggcc gctcaactaa ttaggcctgc accatgactc

40

&lt;210&gt; 50

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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 cttatcgaaa ttaatacgac tcactatagg 30  
  
 <210> 51  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
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 atagattgct ccaaacactt ggtgg 25  
  
 <210> 52  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
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 actccatagg aaaagccgtt cacc 24  
  
 <210> 53  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
 <400> 53  
 gcgagctcta gcatttaggt gacactatag 30  
  
 <210> 54  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
  
 <400> 54  
 ctccaccaag tgtttggtgg tgccttcaga aca 33  
  
 <210> 55  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note = synthetic construct  
 <400> 55  
 Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr  
 1 5 10  
 <210> 56  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
 <400> 56  
 cttatcgaaa ttaatacgac tcactatagg 30  
 <210> 57  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
 <400> 57  
 gaattcgtct cacttccttt cttaaaccag ttgagcttc 39  
 <210> 58  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
 <400> 58  
 ggaattcgtc tcggaagcac gctgggcaag g 31  
 <210> 59  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of artificial sequence; note = synthetic construct  
 <400> 59  
 gcgagctcta gcatttaggt gacactatag 30  
 <210> 60  
 <211> 33

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 60

aactggttta agaaaggaag cacgctgggc gcc

33

<210> 61

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala  
1 5 10